

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/526,508
Source: PT
Date Processed by STIC: 3-13-05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 03/13/2005

PATENT APPLICATION: US/10/526,508

TIME: 12:06:00

Input Set : A:\Sequence listing as filed.txt

Output Set: N:\CRF4\03132005\J526508.raw

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3 <110> APPLICANT: \ABURATANI, Hiroyuki
4     MIDORIKAWA, Yutaka
5     NAKANO, Kiyotaka
6     OHIZUMI, Iwao
7     ITO, Yukio
8     TOKITA, Susumu
10 <120> TITLE OF INVENTION: METHOD FOR DIAGNOSING CANCER BY DETECTING GPC3
W--> 0 <130> FILE REFERENCE:
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/526,508
C--> 13 <141> CURRENT FILING DATE: 2005-03-04
15 <150> PRIOR APPLICATION NUMBER: PCT/JP02/08997
16 <151> PRIOR FILING DATE: 2002-09-04
18 <160> NUMBER OF SEQ ID NOS: 6
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 31
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
30 <400> SEQUENCE: 1
31 gatatacatgg ccgggaccgt gcgcaccgcg t 31
33 <210> SEQ ID NO: 2
34 <211> LENGTH: 31
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial Sequence
38 <220> FEATURE:
39 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
41 <400> SEQUENCE: 2
42 gctagctcag tgcaccagga agaagaagca c 31
44 <210> SEQ ID NO: 3
45 <211> LENGTH: 2300
46 <212> TYPE: DNA
47 <213> ORGANISM: Homo sapiens
49 <220> FEATURE:
50 <221> NAME/KEY: CDS
51 <222> LOCATION: (109)..(1851)
53 <400> SEQUENCE: 3
54 cagcacgtct cttgtctctc agggccactg ccaggcttgc cgagtcttgg gactgctctc 60
55 gctccggctg ccactctccc gcgtctctct agctccctgc gaagcagg atg gcc ggg 117
56                                     Met Ala Gly
57                                     1
58 acc gtg cgc acc gcg tgc ttg gtg gtg gcg atg ctg ctc agc ttg gac 165

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59 Thr Val Arg Thr Ala Cys Leu Val Val Ala Met Leu Leu Ser Leu Asp
60      5      10      15
61 ttc ccg gga cag gcg cag ccc ccg ccg ccg ccg gac gcc acc tgt 213
62 Phe Pro Gly Gln Ala Gln Pro Pro Pro Pro Pro Pro Asp Ala Thr Cys
63 20      25      30      35
64 cac caa gtc cgc tcc ttc ttc cag aga ctg cag ccc gga ctc aag tgg 261
65 His Gln Val Arg Ser Phe Phe Gln Arg Leu Gln Pro Gly Leu Lys Trp
66      40      45      50
67 gtg cca gaa act ccc gtg cca gga tca gat ttg caa gta tgt ctc cct 309
68 Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val Cys Leu Pro
69      55      60      65
70 aag ggc cca aca tgc tgc tca aga aag atg gaa gaa aaa tac caa cta 357
71 Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys Tyr Gln Leu
72      70      75      80
73 aca gca cga ttg aac atg gaa cag ctg ctt cag tct gca agt atg gag 405
74 Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala Ser Met Glu
75      85      90      95
76 ctc aag ttc tta att att cag aat gct gcg gtt ttc caa gag gcc ttt 453
77 Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln Glu Ala Phe
78 100      105      110      115
79 gaa att gtt gtt cgc cat gcc aag aac tac acc aat gcc atg ttc aag 501
80 Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala Met Phe Lys
81      120      125      130
82 aac aac tac cca agc ctg act cca caa gct ttt gag ttt gtg ggt gaa 549
83 Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe Val Gly Glu
84      135      140      145
85 ttt ttc aca gat gtg tct ctc tac atc ttg ggt tct gac atc aat gta 597
86 Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp Ile Asn Val
87      150      155      160
88 gat gac atg gtc aat gaa ttg ttt gac agc ctg ttt cca gtc atc tat 645
89 Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro Val Ile Tyr
90      165      170      175
91 acc cag cta atg aac cca ggc ctg cct gat tca gcc ttg gac atc aat 693
92 Thr Gln Leu Met Asn Pro Gly Leu Pro Asp Ser Ala Leu Asp Ile Asn
93 180      185      190      195
94 gag tgc ctc cga gga gca aga cgt gac ctg aaa gta ttt ggg aat ttc 741
95 Glu Cys Leu Arg Gly Ala Arg Arg Asp Leu Lys Val Phe Gly Asn Phe
96      200      205      210
97 ccc aag ctt att atg acc cag gtt tcc aag tca ctg caa gtc act agg 789
98 Pro Lys Leu Ile Met Thr Gln Val Ser Lys Ser Leu Gln Val Thr Arg
99      215      220      225
100 atc ttc ctt cag gct ctg aat ctt gga att gaa gtg atc aac aca act 837
101 Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile Glu Val Ile Asn Thr Thr
102      230      235      240
103 gat cac ctg aag ttc agt aag gac tgt ggc cga atg ctc acc aga atg 885
104 Asp His Leu Lys Phe Ser Lys Asp Cys Gly Arg Met Leu Thr Arg Met
105      245      250      255
106 tgg tac tgc tct tac tgc cag gga ctg atg atg gtt aaa ccc tgt ggc 933
107 Trp Tyr Cys Ser Tyr Cys Gln Gly Leu Met Met Val Lys Pro Cys Gly

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108	260				265				270				275				
109	ggt	tac	tgc	aat	gtg	gtc	atg	caa	ggc	tgt	atg	gca	ggt	gtg	gtg	gag	981
110	Gly	Tyr	Cys	Asn	Val	Val	Met	Gln	Gly	Cys	Met	Ala	Gly	Val	Val	Glu	
111					280				285				290				
112	att	gac	aag	tac	tgg	aga	gaa	tac	att	ctg	tcc	ctt	gaa	gaa	ctt	gtg	1029
113	Ile	Asp	Lys	Tyr	Trp	Arg	Glu	Tyr	Ile	Leu	Ser	Leu	Glu	Glu	Leu	Val	
114					295				300				305				
115	aat	ggc	atg	tac	aga	atc	tat	gac	atg	gag	aac	gta	ctg	ctt	ggt	ctc	1077
116	Asn	Gly	Met	Tyr	Arg	Ile	Tyr	Asp	Met	Glu	Asn	Val	Leu	Leu	Gly	Leu	
117					310				315				320				
118	ttt	tca	aca	atc	cat	gat	tct	atc	cag	tat	gtc	cag	aag	aat	gca	gga	1125
119	Phe	Ser	Thr	Ile	His	Asp	Ser	Ile	Gln	Tyr	Val	Gln	Lys	Asn	Ala	Gly	
120					325				330				335				
121	aag	ctg	acc	acc	act	att	ggc	aag	tta	tgt	gcc	cat	tct	caa	caa	cgc	1173
122	Lys	Leu	Thr	Thr	Thr	Ile	Gly	Lys	Leu	Cys	Ala	His	Ser	Gln	Gln	Arg	
123	340								345				350			355	
124	caa	tat	aga	tct	gct	tat	tat	cct	gaa	gat	ctc	ttt	att	gac	aag	aaa	1221
125	Gln	Tyr	Arg	Ser	Ala	Tyr	Tyr	Pro	Glu	Asp	Leu	Phe	Ile	Asp	Lys	Lys	
126									360				365			370	
127	gta	tta	aaa	ggt	gct	cat	gta	gaa	cat	gaa	gaa	acc	tta	tcc	agc	cga	1269
128	Val	Leu	Lys	Val	Ala	His	Val	Glu	His	Glu	Glu	Thr	Leu	Ser	Ser	Arg	
129									375				380			385	
130	aga	agg	gaa	cta	att	cag	aag	ttg	aag	tct	ttc	atc	agc	ttc	tat	agt	1317
131	Arg	Arg	Glu	Leu	Ile	Gln	Lys	Leu	Lys	Ser	Phe	Ile	Ser	Phe	Tyr	Ser	
132									390				395			400	
133	gct	ttg	cct	ggc	tac	atc	tgc	agc	cat	agc	cct	gtg	gcg	gaa	aac	gac	1365
134	Ala	Leu	Pro	Gly	Tyr	Ile	Cys	Ser	His	Ser	Pro	Val	Ala	Glu	Asn	Asp	
135									405				410			415	
136	acc	ctt	tgc	tgg	aat	gga	caa	gaa	ctc	gtg	gag	aga	tac	agc	caa	aag	1413
137	Thr	Leu	Cys	Trp	Asn	Gly	Gln	Glu	Leu	Val	Glu	Arg	Tyr	Ser	Gln	Lys	
138	420								425				430			435	
139	gca	gca	agg	aat	gga	atg	aaa	aac	cag	ttc	aat	ctc	cat	gag	ctg	aaa	1461
140	Ala	Ala	Arg	Asn	Gly	Met	Lys	Asn	Gln	Phe	Asn	Leu	His	Glu	Leu	Lys	
141									440				445			450	
142	atg	aag	ggc	cct	gag	cca	gtg	gtc	agt	caa	att	att	gac	aaa	ctg	aag	1509
143	Met	Lys	Gly	Pro	Glu	Pro	Val	Val	Ser	Gln	Ile	Ile	Asp	Lys	Leu	Lys	
144									455				460			465	
145	cac	att	aac	cag	ctc	ctg	aga	acc	atg	tct	atg	ccc	aaa	ggt	aga	gtt	1557
146	His	Ile	Asn	Gln	Leu	Leu	Arg	Thr	Met	Ser	Met	Pro	Lys	Gly	Arg	Val	
147									470				475			480	
148	ctg	gat	aaa	aac	ctg	gat	gag	gaa	ggg	ttt	gaa	agt	gga	gac	tgc	ggt	1605
149	Leu	Asp	Lys	Asn	Leu	Asp	Glu	Glu	Gly	Phe	Glu	Ser	Gly	Asp	Cys	Gly	
150									485				490			495	
151	gat	gat	gaa	gat	gag	tgc	att	gga	ggc	tct	ggt	gat	gga	atg	ata	aaa	1653
152	Asp	Asp	Glu	Asp	Glu	Cys	Ile	Gly	Gly	Ser	Gly	Asp	Gly	Met	Ile	Lys	
153	500								505				510			515	
154	gtg	aag	aat	cag	ctc	cgc	ttc	ctt	gca	gaa	ctg	gcc	tat	gat	ctg	gat	1701
155	Val	Lys	Asn	Gln	Leu	Arg	Phe	Leu	Ala	Glu	Leu	Ala	Tyr	Asp	Leu	Asp	
156									520				525			530	

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158 Val Asp Asp Ala Pro Gly Asn Ser Gln Gln Ala Thr Pro Lys Asp Asn
159      535      540      545
160 gag ata agc acc ttt cac aac ctc ggg aac gtt cat tcc ccg ctg aag 1797
161 Glu Ile Ser Thr Phe His Asn Leu Gly Asn Val His Ser Pro Leu Lys
162      550      555      560
163 ctt ctc acc agc atg gcc atc tgc gtg gtg tgc ttc ttc ttc ctg gtg 1845
164 Leu Leu Thr Ser Met Ala Ile Ser Val Val Cys Phe Phe Phe Leu Val
165      565      570      575
166 cac tga ctgcctggtg cccagcacat gtgctgccct acagcaccct gtggtcttcc 1901
167 His
168 580
169 tcgataaagg gaaccacttt cttatTTTTT tctatTTTTT tttttttggt atcctgtata 1961
170 cctcctccag ccatgaagta gaggactaac catgtgttat gttttcgaaa atcaaattggt 2021
171 atctttttgga ggaagataca ttttagtggt agcatataga ttgtcctttt gcaaagaaag 2081
172 aaaaaaaaaacc atcaagttgt gccaaattat tctcctatgt ttggtctgta gaacatggtt 2141
173 accatgtctt tctctctcac tccctccctt tctatcgttc tctctttgca tggatttctt 2201
174 tgaaaaaaaaa taaattgctc aaataaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2261
175 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2300
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178 <211> LENGTH: 580
179 <212> TYPE: PRT
180 <213> ORGANISM: Homo sapiens
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185 Ser Leu Asp Phe Pro Gly Gln Ala Gln Pro Pro Pro Pro Pro Pro Asp
186 20 25 30
187 Ala Thr Cys His Gln Val Arg Ser Phe Phe Gln Arg Leu Gln Pro Gly
188 35 40 45
189 Leu Lys Trp Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val
190 50 55 60
191 Cys Leu Pro Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys
192 65 70 75 80
193 Tyr Gln Leu Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala
194 85 90 95
195 Ser Met Glu Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln
196 100 105 110
197 Glu Ala Phe Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala
198 115 120 125
199 Met Phe Lys Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe
200 130 135 140
201 Val Gly Glu Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp
202 145 150 155 160
203 Ile Asn Val Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro
204 165 170 175
205 Val Ile Tyr Thr Gln Leu Met Asn Pro Gly Leu Pro Asp Ser Ala Leu
206 180 185 190
207 Asp Ile Asn Glu Cys Leu Arg Gly Ala Arg Arg Asp Leu Lys Val Phe

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208          195          200          205
209 Gly Asn Phe Pro Lys Leu Ile Met Thr Gln Val Ser Lys Ser Leu Gln
210          210          215          220
211 Val Thr Arg Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile Glu Val Ile
212 225          230          235          240
213 Asn Thr Thr Asp His Leu Lys Phe Ser Lys Asp Cys Gly Arg Met Leu
214          245          250          255
215 Thr Arg Met Trp Tyr Cys Ser Tyr Cys Gln Gly Leu Met Met Val Lys
216          260          265          270
217 Pro Cys Gly Gly Tyr Cys Asn Val Val Met Gln Gly Cys Met Ala Gly
218          275          280          285
219 Val Val Glu Ile Asp Lys Tyr Trp Arg Glu Tyr Ile Leu Ser Leu Glu
220          290          295          300
221 Glu Leu Val Asn Gly Met Tyr Arg Ile Tyr Asp Met Glu Asn Val Leu
222 305          310          315          320
223 Leu Gly Leu Phe Ser Thr Ile His Asp Ser Ile Gln Tyr Val Gln Lys
224          325          330          335
225 Asn Ala Gly Lys Leu Thr Thr Thr Ile Gly Lys Leu Cys Ala His Ser
226          340          345          350
227 Gln Gln Arg Gln Tyr Arg Ser Ala Tyr Tyr Pro Glu Asp Leu Phe Ile
228          355          360          365
229 Asp Lys Lys Val Leu Lys Val Ala His Val Glu His Glu Glu Thr Leu
230          370          375          380
231 Ser Ser Arg Arg Arg Glu Leu Ile Gln Lys Leu Lys Ser Phe Ile Ser
232 385          390          395          400
233 Phe Tyr Ser Ala Leu Pro Gly Tyr Ile Cys Ser His Ser Pro Val Ala
234          405          410          415
235 Glu Asn Asp Thr Leu Cys Trp Asn Gly Gln Glu Leu Val Glu Arg Tyr
236          420          425          430
237 Ser Gln Lys Ala Ala Arg Asn Gly Met Lys Asn Gln Phe Asn Leu His
238          435          440          445
239 Glu Leu Lys Met Lys Gly Pro Glu Pro Val Val Ser Gln Ile Ile Asp
240          450          455          460
241 Lys Leu Lys His Ile Asn Gln Leu Leu Arg Thr Met Ser Met Pro Lys
242 465          470          475          480
243 Gly Arg Val Leu Asp Lys Asn Leu Asp Glu Glu Gly Phe Glu Ser Gly
244          485          490          495
245 Asp Cys Gly Asp Asp Glu Asp Glu Cys Ile Gly Gly Ser Gly Asp Gly
246          500          505          510
247 Met Ile Lys Val Lys Asn Gln Leu Arg Phe Leu Ala Glu Leu Ala Tyr
248          515          520          525
249 Asp Leu Asp Val Asp Asp Ala Pro Gly Asn Ser Gln Gln Ala Thr Pro
250          530          535          540
251 Lys Asp Asn Glu Ile Ser Thr Phe His Asn Leu Gly Asn Val His Ser
252 545          550          555          560
253 Pro Leu Lys Leu Leu Thr Ser Met Ala Ile Ser Val Val Cys Phe Phe
254          565          570          575
255 Phe Leu Val His
256          580

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VERIFICATION SUMMARY

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L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date